```
AMSH1    THNEFTITHVIVP--KQSAGPDYCDMKNVEELJNVQDQHD--LLTLGWIFTFPTQTAFLS
AMSH2    THNEFTITHVIVP--KQSAGPDYCDMKNVEELJNVQDQHD--LLTLGWIFTFPTQTAFLS
AMSH     MRNEFTITHVLIP--KQSAGSDYCNTENEEELJLIQDQQG--LITLGWIFTFPTQTAFLS
Rpn11    TVRVIDVFAMPQS--GTGVSVEAVDPVFQAKMLDHLXQTGRPXMVVGHYYSHFGFGCWLS
Jab1     TMIIMDSFALPVEGTETRVNAQAAAYEYMAAYIENAXQVGRLENAIGHYYSHPGYGCWLS
                :       :         .. :        :     .*.     .:**   :#:*    .:**

AMSH1    SVFLHTHCSYQIMLPEAIAIVCSFKHKDTG-----IFRLTNAGMLEVSACKKKGFH--PH
AMSH2    SVFLHTHCSYQIMLPEAIAIVCSFKHKDTG-----IFRLTNAGMLEVSACKKKGFH--PH
AMSH     SVDLHTHCSYQMMLPESVAIVCSFKFQETG-----FFKLTDHGLXEISSCRQKGFH--PH
Rpn11    GVFINTQQSFEALSERAVAVVVDPIQSVKGKVVIDAFRLINANMMVLGHFPRQTTSNIGH
Jab1     GIFVSTQMLNQQFQEPFVAVVIDPTRTISAG----KVNLGAFRTYPKGYKPPDEGPSFYQ
          .:#: *: :    : :  :  :*#:*.* :      ..*         .      .      :

AMSH1    TKEPRLFSICKHV--LVKDIKI----------IVLDLR--------------------
AMSH2    TKEPRLFSIQKFLSGIISGTAL----------KHEPLXIGYGPNGFPLLGISRSSSPSEQ
AMSH     SKDPPLFCSCSHVT--VVDRAV----------TITDLR--------------------
Rpn11    LNKPSIQALIHGLNRHYYSITINYRKNELXQKMLLNLHKRSHMEGLTLQDYSEHCKHNIS
Jab1     TIPLNKIEDFGVHCKQYYALEVSYFKSSLDRKLLELLFNKYWVNTLSSSSLLTNADYTTG
                                          :            : *

AMSH1    ---------------------------------------------------------
AMSH2    L--------------------------------------------------------
AMSH     ---------------------------------------------------------
Rpn11    VVKEMLELAKNYRKAVEKEDKHTPFEQIAIKNVGKQDPKRHLETHVDVLMTSNIVQCLAAM
Jab1     QVFDLSEKIEQSEAQLGRGSFMLG--LETHDRKSEDKLAKATRDSCKTTIEAIHGLMSQV

AMSH1    -----------
AMSH2    -----------
AMSH     -----------
Rpn11    LDTVVFK-----
Jab1     IKDKLFRQINIS
```

FIGURE 1

```
AMSH1    ---------------MFDHTDVSLSPEERVRALSKLGCNITISEDITPRR  35
AMSH2    MDQPFTVNSLKKLAAMPDHTDVSLSPEERVRALSKLGCNITISEDITPRR  50
AMSH     ---------------MSDHGDVSLPFEDRVRALSQLGSAVEVNEDIPPRR  35
                        *.** **** .**.**,***** *;,**, ; ;,.***.***

AMSH1    YFRSGVEMIRMASVYLEIGNIENAFVLYNKFITLFVEKLFNHRDYQQCAV  85
AMSH2    YFRSGVEMIRMASVYLEIGNIENAFVLYNKFITLFVEKLFNHRDYQQCAV 100
AMSH     YFRSGVEIIRMASIYSEEGNIEHAFILYNKYITLFIEKLPKHRDYKSAVI  85
                *******;; ****;,* ****;*;,** ,****;****;.******;,...;

AMSH1    PEKQDIMKKLKEIAFPRTDELRNDLLEKYNVEYQEYLQSKNKYKAEILKK 135
AMSH2    PEKQDIMKKLKEIAFPRTDELRNDLLEKYNVEYQEYLQSKNKYKAEILKK 150
AMSH     PEKKDTVKRLKEIAFPKAEELKAELLKRYTKEYTEYNEEKKKIAEELARN 135
                ***;* ,*********;;;*** ;***;*. ** ** ;.*;*   *; ;;

AMSH1    LEHQRLIEAERKRIAQMRQQQLESEQFLFFEDQLKKQELARGQMRSQQTS 185
AMSH2    LEHQRLIEAERKRIAQMRQQQLESEQFLFFEDQLKKQELARGQMRSQQTS 200
AMSH     MAIQQELEKEKQRVAQQKQQQLEQEQFHAFEEMIRNQELEKERLKIVQEF 185
                ;    *;  ;*   *;;*;** ;*****;.*** **;  ***;***  ; ;;;     *

AMSH1    G-LSEQIDGSALSCFS--THQNNSLLNVFADQPNKSDATNYASHSPPVNR 232
AMSH2    G-LSEQIDGSALSCFS--THQNNSLLNVFADQPNKSDATNYASHSPPVNR 247
AMSH     GKVDPGLGGPLVPDLEKPSLDVFPTLTVSSIQPSDCHTTVRPAKPPVVDR 235
                * ;.   ;.*.;. ;.    ;;    .  *.*; ; **....;*  .;;.* ;;*

AMSH1    ALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGIL 282
AMSH2    ALTPAATLSAVQNLVVEGLRCVVLPEDLCHKFLQLAESNTVRGIETCGIL 297
AMSH     SLKPGALSNSESIPTIDGLRHVVVPGRLCPQFLQLASANTARGVETCGIL 285
                ;*.*.*   .;;   ..;;*** **;* ** ;*****.;**.**;*****;

AMSH1    CGKLTHNEFTITHVIVPKQSAGPDYCDMENVEELFNVQDQHDLLTLGWII 332
AMSH2    CGKLTHNEFTITHVIVFKQSAGPDYCDMENVEELFNVQDQHDLLTLGWII 347
AMSH     CGKLMRNEFTITHVLIPKQSAGSDYCNTENEEELFLIQDQQGLITLGWII 335
                ****;*********;;;******.***; ** **** ;***;.*;*****

AMSH1    TPTQTAFLSSVLHTHCSYQLMLFEAIAIVCSPKHRDTGIFRLTNAGML 382
AMSH2    TPTQTAFLSSVLHTHCSYQLMLFEAIAIVCSPKHKDTGIFRLTNAGML 397
AMSH     TPTQTAFLSSVLHTHCSYQMMLPESVAIVCSPKFQETGFFKLTDHGLE 385
                 ;********** ;*********;,;***;;,*******;.;;**;*;**;  *;

AMSH1    EVSACKKKGFHPHTKEPRLFSICKHV--LVKDIKIIVLDLR--------- 421
AMSH2    EVSACKKKGFHPHTKEPRLFSIQKFLSGIISGTALEMEPLKIGYGFNGFP 447
AMSH     EISSCRQKGFHFHSKDPPLFCSCSHVT--VVDRAVTITDLR--------- 424
                *;*;*;;*******;*;* **.  ..;   ;  . ; ;  *;

AMSH1    ---------------
AMSH2    LLGISRSSSPSEQL  461
AMSH     ---------------
```

FIGURE 2

```
COP9_su5_Hs      VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm      VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At      AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVEIG
COP9_su5_Ce      EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
AF2198_Arcfu     LPIGMKVFGTVHSHPSPSCRPSEEDLSLFTRFGKYHIIVCY--PYDENSWKCYNRKGEEV
PH0451_Pyrho     MPHDESIKGTFHSHPSPFPYPSEGDIMFFSKFGGIHIIAAF--PYDEDSVKAFDSEGREV
TVN1035_Thevo    KPIDFSLVGSVHSHPSGITKPSDEDLRMFSLTGKIHIIVGY--PYNLKDYSAYDRSGNKV
MTH971_Metth     LPPFTGAVGSVHSHPGPVNLPSAADLHFFSKNGLFHLIIAH--PYTMETVAAYTRNGDPV
aq_1691_Aquae    ISKGMEIVGVYHSHPDHPDRPSQFDLQRAFPDLSYIIFSVQ--KGKVASYRSWELKGDKF
RV1334_Myctu     EDADEVPVVIYHSHTATEAYPSRTDVKLATEPDAHYVLVSTRDPHRHELRSYRIVDGAVT
RadC_Ecoli       IKINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA
                 ''''''''''''''''''''''''''''''HSHP''''''S''D
```

FIGURE 3

```
COP9_su5_Hs   VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTISAGKVNLG
COP9_su5_Dm   VGRMEHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_su5_At   AGRLENVVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVBIG
COP9_su5_Ce   EGRKEKVVGWYHSHPGYGCWLSGIDVSTQTLNQKFQEPWVA--IVIDPLRTMSAGKVDIG
Pad1_Dm       TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Pad1_Hs       TGRPEMVVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPIQSVKG-KVVID
Sks1_Dd       TGFDEIVIGWYHSHPGFGCWLSSVDVNTQQSFEQLQSRAVA--VVVDPLQSVRG-KVVID
Pad1_Sc       TGRDQMVVGWYHSHPGFGCWLSSVDVNTQKSFEQLNSRAVA--VVVDPIQSVKG-KVVID
              ''''''''''''''''''''''''''  HSHP''''''S 'D
```

FIGURE 4